

SEQUENCE LISTING

<110> Simard, John J. L.
Diamond, David C.

<120> EPITOPE SYNCHRONIZATION IN ANTIGEN
PRESENTING CELLS

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<150> 09/561,074

<151> 2000-04-28

<150> 09/560,465

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<150> 09/561,572

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<151> 2000-04-28

<150> PCT/US01/13806

<151> 2001-04-27

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Leu Thr Val Ile Leu Gly Val Leu Leu Leu Ile Gly Cys Trp Tyr Cys
      35             40             45
Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val
      50             55             60
Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp
      65             70             75             80
His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
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Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
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Pro Pro Pro Tyr Ser Pro
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35 40 45
Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
50 55 60
Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65 70 75 80
Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
85 90 95
Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
100 105 110
Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
115 120 125
Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
130 135 140
Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
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Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
180 185

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Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45
Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60
His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Arg Cys Gly Ala
65 70 75 80
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
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Gly Gln Arg Arg
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35 40 45
Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50 55 60
Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80
Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95
Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
100 105 110
Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
115 120 125
Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
130 135 140
Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145 150 155 160
Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165 170 175
Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Ser
180 185 190
Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
195 200 205
Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
210 215 220
Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
225 230 235 240
Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Met Gly Gly Gln His
245 250 255
Pro Thr Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
260 265 270
Gln Ile Val Cys Ser Arg Leu Glu Glu Tyr Asn Ser His Gln Ser Leu
275 280 285
Cys Asn Gly Thr Pro Glu Gly Pro Leu Arg Arg Asn Pro Gly Asn His
290 295 300
Asp Lys Ser Arg Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
305 310 315 320
Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Lys Ala Ala
325 330 335
Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
340 345 350
Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile
355 360 365
Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro

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370 375 380
 Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
 385 390 395 400
 Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
 405 410 415
 Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
 420 425 430
 Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
 435 440 445
 Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
 450 455 460
 Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
 465 470 475 480
 Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
 485 490 495
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 caaagattga tctttgccgg taagcagcta gaagacggta gaacgctgtc tgattacaac 180
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 gggcccggaa acctggccct gtcttcttga cgagcattcc taggggtctt tcccctctcg 180
 ccaaaggaat gcaaggtctg ttgaatgtcg tgaaggaagc agttcctctg gaagcttctt 240
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 ggtgcctctg cggccaaaag ccacgtgtat aagatacacc tgcaaaggcg gcacaacccc 360
 agtgccacgt tgtgagttgg atagttgtgg aaagagtcaa atggctctcc tcaagcgtat 420
 tcaacaaggg gctgaaggat gccagaagg taccctattg tatgggatct gatctggggc 480
 ctcggtgcac atgctttaca tgtgtttagt cgagggttaa aaaacgtcta ggccccccga 540
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